AMENDMENTS TO THE SPECIFICATION

Please amend the following paragraphs as follows:

[0133]The immobilized DNAs are a Maf recognition sequence (MARE 25) (SEQ ID NO:6) and a Maf non-recognition sequence (MARE 23) (SEQ ID NO:9), their details of which are shown in FIGS. 2 and 1, respectively. Each of the sequences is designed such that a purposive sequence is linked to a 5' thiol terminal through a thymine 15-base spacer.

[0138] The observation was performed at three points: two regions each having the immobilized MARE 25 (SEQ ID NO:6) or MARE 23 (SEQ ID NO:9), and one region having no DNA (background position). FIG. 4 shows the change of the SPR signal. It can be observed that the MafG homodimer is bonded only to the sequence of MARE 25 (SEQ ID NO:6), and substantially no MafG homodimer is bonded to MARE and the background position. An association rate constant, a dissociation rate constant and an association equilibrium constant were 2.22×10^5 (M^{-1} s^{-1}), 8.80×10^{-4} (s^{-1}) and 2.52×10^8 (M^{-1}), respectively.

[0139] The difference between one image picked up before supplying the MafG homodimer into the cell, and another image picked up ten minutes after completion of the

supply was evaluated by processing these images using an image processing software NIT Image. FIG. 5 shows this result. As seen in FIG. 5, the MafG homodimer is bonded only to the sequence of MARE 25 (SEQ ID NO:6).

[0142] Then, respective single-stranded DNAs of MARE 25 (SEQ ID NO:6) ~~sequence~~ and MARE 23 (SEQ ID NO:9) sequences each having thiol at its 5' terminal were dissolved in a 1mM phosphoric acid buffer solution. Then, the mixture was spotted on the surface in an array arrangement to immobilize the single-stranded DNAs on the surface through reaction with the surface for 15 hours.

[0143] After the surface with the immobilized DNAs was rinsed with a phosphoric acid buffer solution, the substrate was set up in the SPR imaging apparatus, and the flow cell was filled with the transfer-factor-measuring buffer solution. Then, a DNA complementary to MARE 25 (SEQ ID NO:6) was added into the cell at a concentration of 1 μM, and left for 20 minutes to hybridize the complementary DNA to MARE 25 (SEQ ID NO:6). After rinsing the surface, a DNA complementary to MARE 23 (SEQ ID NO:9) was added into the cell at a concentration of 1 μM, and left for 20 minutes to hybridize the complementary DNA to MARE 23 (SEQ ID NO:9).

[0144] The interaction with the MafG homodimer was observed through the same process as in Inventive Example 1. As a result, the MafG homodimer was absorbed to both MARE 25 (SEQ ID NO:6) and MARE 23 (SEQ ID NO:9), and no specificity of the transfer factor MafG could be observed (FIG. 6). This would be caused because the DNA complementary to MARE 25 (SEQ ID NO:6) was also bonded to MARE 23 (SEQ ID NO:9) to preclude the formation of the intended double-stranded DNA.

[0182] FIG. 13 is a graph showing the signal change. In this manner, the interactions at six points on a single chip could be simultaneously observed. In this example, it could be confirmed that the bonding strength to MARE 25 (SEQ ID NO:6) as a consensus sequence is high, and the bonding strength to MARE 23 (SEQ ID NO:9) is low. As seen in FIG. 13, no signal change is observed in the background region (4-arm PEG), which shows that substantially no MafG was bonded thereto. The comparison between the kinetics value obtained from a association/disassociation curve and the value obtained through a gel mobility shift assay (GMSA) as a conventional interaction-measuring method is shown in the following table. While there are some differences between the respective values of SPR and GMSA, the bonding strength could be sufficiently evaluated through the SPR in view of affinity and bonding strength.

Table 3

	SPR average			GMSA
	$ka[m^{-1}s^{-1}]10^{5}$	$Kd[S^{-1}]10^{-4}$	$K_D[M]10^{-9}$	$K_D[M]10^{-7}$
MARE 25 (SEQ ID NO:6)	1.36+/- 0.32	3.13 +/- 0.66	2.50+/- 1.02	2.49 +/- 0.66
hOPSIN	0.493 +/- 0.062	3.72 +/- 0.03	7.67 +/- 1.17	2.52 +/- 0.05
hNQO1m	0.385 +/- 0.035	3.24 +/- 0.36	8.58 +/- 1.75	2.73 +/- 0.13
mGSTY	N.D	N.D	N.D	N.D
MARE23 (SEQ ID NO:9)	N.D	N.D	N.D	N.D
hBglHS4	N.D	N.D	N.D	N.D